pathogen. In another embodiment, the sample pair is represented by undifferentiated cells, e.g., stem cells, and differentiated cells.

[0144] Cells from any organism, e.g., from bacteria, yeast, plants and animals, such as fish, birds, reptiles, amphibians and mammals may be used in the subject method. In certain embodiments, mammalian cells, i.e., cells from mice, rabbits, primates, or humans, or cultured derivatives thereof, may be used.

[0145] All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

EXAMPLES

[0146] The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the present invention, and are not intended to limit the scope of what the inventors regard as their invention nor are they intended to represent that the experiments below are all or the only experiments performed.

Example 1

[0147] Single Cell Mass Tomography from SIMS analysis of arrayed cells

[0148] In implementing the present method, the inherent curvature of the cell may distort the SIMS primary ion beam analysis plane as it burrows through the cell across repeat scans (FIG. **3**, top). Predictable, cell compartment specific mass reporter signatures are attainable by modeling the curved plane and applying cell localization standards (FIG. **3**, bottom).

Example 2

[0149] SIMS depth profile of a single cell reveals relative sub-cellular localization of expressed components

[0150] FIG. **4** shows a low resolution (>1 μm beam size) sequential scan of an immobilized human Jurkat T cell stained with mono isotopic elemental reporters for the surface molecule CD3 and CD45, cytosolic molecule ribosomal protein S6, and nuclear molecule double stranded DNA (sDNA). As each layer of the immobilized cell was ablated and analyzed by the oxygen duoplasmatron beam the normalized expression (Y axis) of the aforementioned molecules changed in a pattern corresponding to their expected localization. First, CD3 and CD45 were at maximal expression, then as the analysis depth into the cell increased (increased plan number—X axis) S6 reached a maximum followed by dsDNA. Visual correlation with the differential expression patterns at the indicated SIMS depth planes were observed, as shown in the inset images.

Example 3

[0151] Correlation analysis reveals localization

[0152] Plotting known reporter signals for cell localization analysis on a scan-by-scan basis revealed co-localization. As shown in FIG. **5**, the NFkB negative regulator IkB alpha was co-localized with cytosolic actin (black arrow).

What is claimed is:

1. A method of analyzing a population of cells, comprising:

i) obtaining an array of cells on a substrate, wherein the cells are labeled with one or more mass tags and are separated from one another;

ii) measuring, using secondary ion mass spectrometry (SIMS), the abundance of the one or more mass tags at a plurality of locations occupied by the cells, thereby generating, for each individual cell measured, a set of data; and

iii) outputting the set of data for each of the cells analyzed.

2. The method of claim **1**, wherein the array is addressable.

3. The method of claim **1**, wherein the array is random and the locations occupied by the cells are determined by imaging the substrate prior to the measuring step.

4. The method of claim **3**, wherein the imaging is by optical imaging, electron imaging or low resolution SIMS.

5. The method of claim **1**, wherein the measuring step comprises applying a SIMS ion beam with a diameter equal to or greater than half the average diameter of individual cells to measure the abundance of the one or more mass tags on a whole cell basis.

6. The method of claim **5**, wherein the SIMS ion beam has a diameter in the range of 1 μm to 50 μm.

7. The method of claim **1**, wherein the measuring step comprises applying a plurality of pulses of a SIMS ion beam at different sites of an individual cell of the array to obtain measurements of the abundance of the one or more mass tags at the different sites.

8. The method of claim **7**, wherein the SIMS ion beam has a diameter in the range of 10 nm to 1500 nm.

9. The method of claim **8**, wherein the method comprises measuring the abundance of said one or more mass tags at a plurality of depths as the SIMS ion beam etches through the individual cell.

10. The method of claim **1**, wherein the array of cells is obtained by:

labeling cells with one or more mass tags; and

attaching cells to a substrate;

wherein the labeling is done either prior to or after the cells are attached to the substrate.

11. The method of claim **10**, wherein said labeling is done by administering the mass tag to an animal subject and obtaining labeled cells from said subject.

12. The method of claim **1**, wherein the method comprises:

labeling cells with a first mass tag and a second mass tag, wherein the first mass tag localizes to a known subcellular structure of the cell;

measuring the abundance of the first and second mass tags at different sites of an individual cell of the array; and

determining the subcellular localization of the second mass tag based on the measured abundance of the first and second mass tags.

13. The method of claim **1**, further comprising:

iv) identifying one or more cells of interest based on the obtained set of data; and

v) recovering the identified cells for further analysis.

14. The method of claim **5**, further comprising:

identifying one or more cells of interest based on the obtained set of data;